



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 01:54 PM GMT

PDB ID : 1M1X  
Title : CRYSTAL STRUCTURE OF THE EXTRACELLULAR SEGMENT OF INTEGRIN ALPHA VBETA3 BOUND TO MN2+  
Authors : Xiong, J.-P.; Stehle, T.; Zhang, R.; Joachimiak, A.; Frech, M.; Goodman, S.L.; Arnaout, M.A.  
Deposited on : 2002-06-20  
Resolution : 3.30 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

---

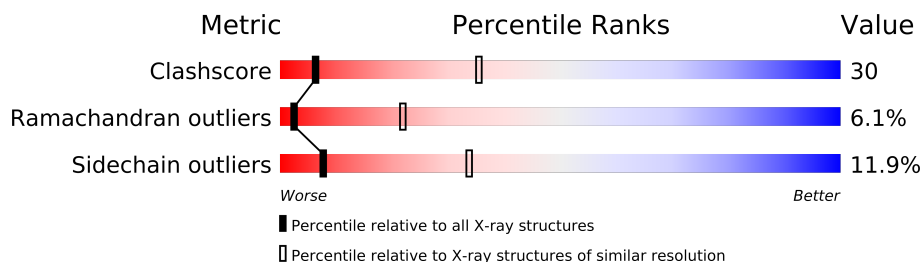
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1696 (3.40-3.20)
Ramachandran outliers	78287	1664 (3.40-3.20)
Sidechain outliers	78261	1662 (3.40-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	957	
2	B	692	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11656 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Integrin alpha-V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	927	Total	C	N	O	S	0	0	0
			7216	4568	1224	1389	35			

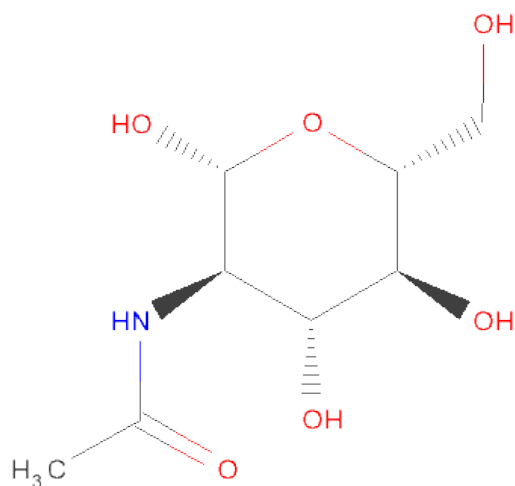
- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	539	Total	C	N	O	S	0	0	0
			4182	2594	700	842	46			

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		
5	B	2	Total	C	N	O	0	0
			28	16	2	10		
5	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Mn	0	0
			1	1		
6	A	5	Total	Mn	0	0
			5	5		

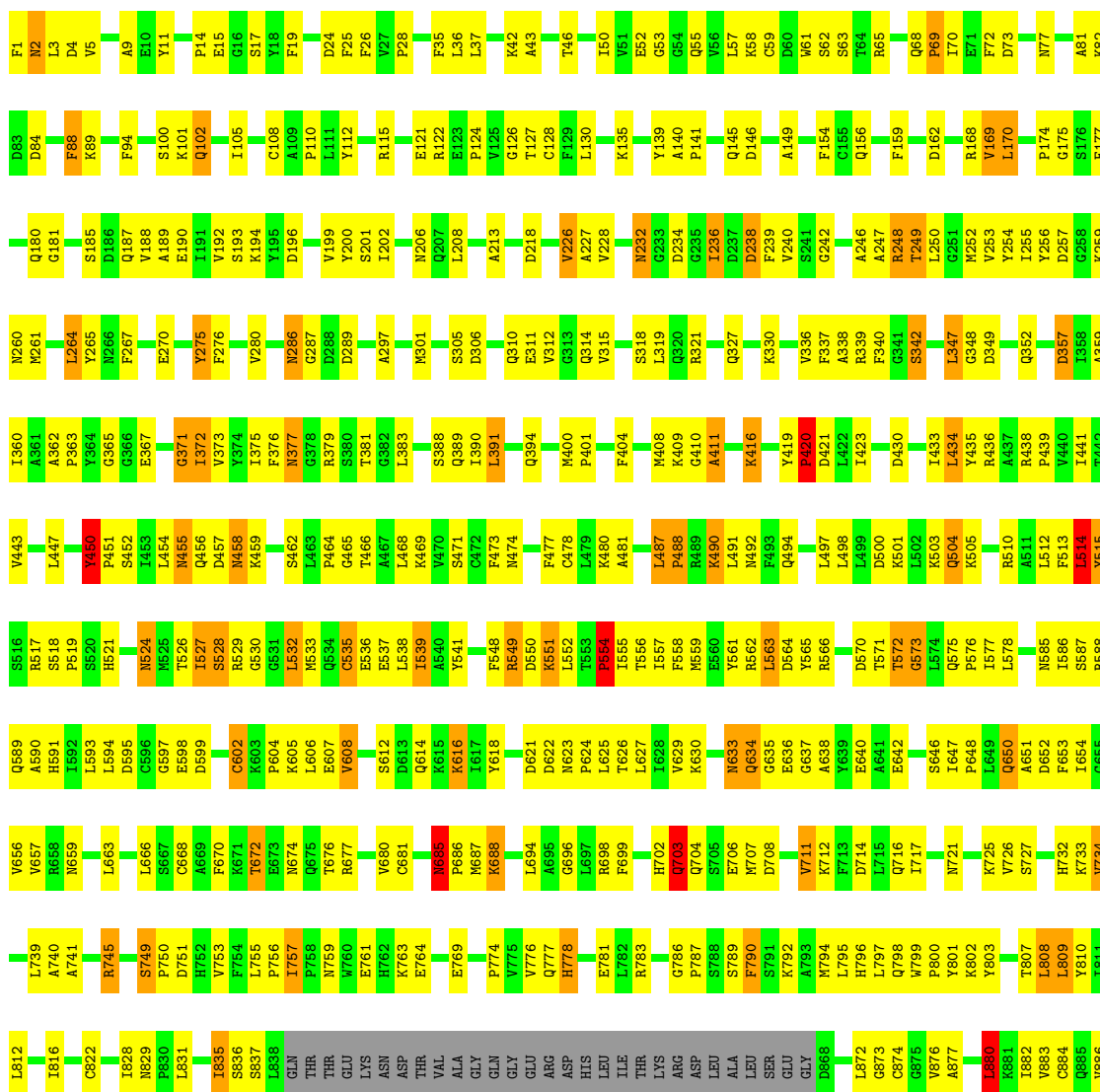
### 3 Residue-property plots

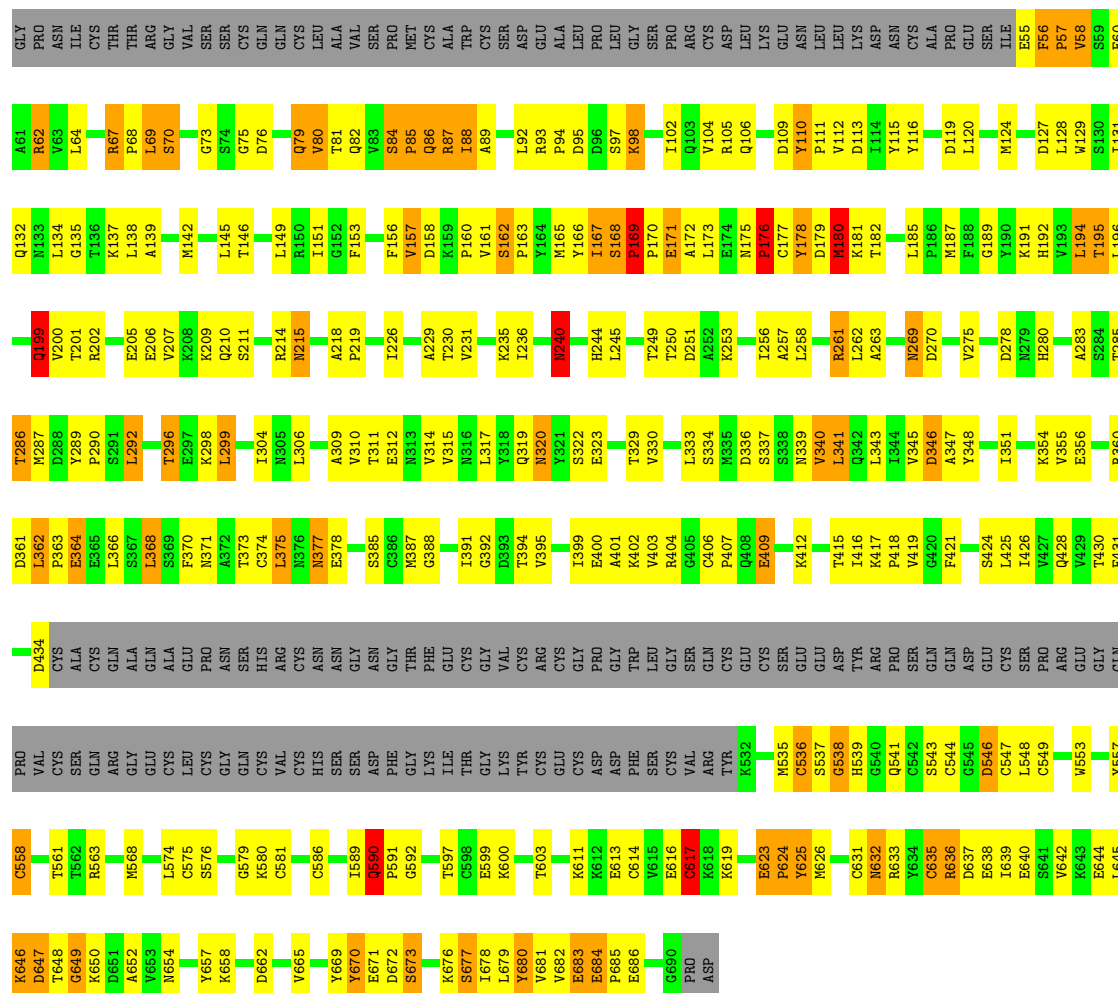
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

#### • Molecule 1: Integrin alpha-V

Chain A:





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	130.40Å 130.40Å 310.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.30	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-3.30)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.244 , 0.323	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11656	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, NAG, NDG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.47	0/7372	0.79	7/9994 (0.1%)
2	B	0.46	0/4256	0.80	4/5754 (0.1%)
All	All	0.46	0/11628	0.79	11/15748 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	912	GLU	N-CA-C	8.13	132.95	111.00
1	A	880	LEU	N-CA-C	-6.37	93.81	111.00
1	A	450	TYR	C-N-CD	6.21	141.45	128.40
2	B	590	GLN	N-CA-C	5.73	126.46	111.00
2	B	180	MET	N-CA-C	-5.71	95.60	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	625	TYR	Sidechain



## 5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7216	0	7036	403	0
2	B	4182	0	4028	279	0
3	A	112	0	100	17	0
4	A	28	0	26	9	0
4	B	28	0	26	10	0
5	A	28	0	25	6	0
5	B	56	0	50	12	0
6	A	5	0	0	0	0
6	B	1	0	0	0	0
All	All	11656	0	11291	694	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 30.

The worst 5 of 694 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:A:2943:NAG:H2	5:A:2943:NAG:H61	1.28	1.14
1:A:753:VAL:HG22	1:A:951:VAL:HG12	1.36	1.07
1:A:800:PRO:HB3	1:A:873:GLY:HA2	1.37	1.04
1:A:685:ASN:HB3	1:A:686:PRO:HD3	1.40	0.98
1:A:585:ASN:ND2	3:A:2585:NAG:H61	1.79	0.97

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	923/957 (96%)	728 (79%)	152 (16%)	43 (5%)	4	30
2	B	535/692 (77%)	407 (76%)	82 (15%)	46 (9%)	1	11
All	All	1458/1649 (88%)	1135 (78%)	234 (16%)	89 (6%)	2	22

5 of 89 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	69	PRO
1	A	82	LYS
1	A	411	ALA
1	A	420	PRO
1	A	450	TYR

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	787/812 (97%)	696 (88%)	91 (12%)	8	35
2	B	484/616 (79%)	424 (88%)	60 (12%)	7	31
All	All	1271/1428 (89%)	1120 (88%)	151 (12%)	8	34

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	703	GLN
1	A	906	GLU
2	B	544	CYS
1	A	711	VAL
1	A	783	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	524	ASN
1	A	650	GLN
2	B	376	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	580	GLN
1	A	685	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

14 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	NAG	A	2044	1,3	12,14,15	0.60	0	15,19,21	0.89	1 (6%)
3	NAG	A	2045	3	12,14,15	0.44	0	15,19,21	0.66	0
3	NAG	A	2266	1,3	12,14,15	0.58	0	15,19,21	0.74	0
3	NAG	A	2267	3	12,14,15	0.37	0	15,19,21	0.79	0
3	NAG	A	2585	1,3	12,14,15	0.45	0	15,19,21	0.78	0
3	NAG	A	2586	3	12,14,15	0.40	0	15,19,21	0.69	0
5	NAG	A	2943	1,5	12,14,15	0.51	0	15,19,21	0.81	0
5	NDG	A	2944	5	12,14,15	0.47	0	15,19,21	0.75	0
3	NAG	A	2950	1,3	12,14,15	0.59	0	15,19,21	0.75	0
3	NAG	A	2951	3	12,14,15	0.43	0	15,19,21	0.63	0
5	NAG	B	3559	2,5	12,14,15	0.49	0	15,19,21	0.65	0
5	NDG	B	3560	5	12,14,15	0.46	0	15,19,21	0.79	0
5	NAG	B	3654	2,5	12,14,15	0.55	0	15,19,21	0.95	0
5	NDG	B	3655	5	12,14,15	0.36	0	15,19,21	0.66	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	2044	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	2045	3	-	0/6/23/26	1/1/1/1
3	NAG	A	2266	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	2267	3	-	0/6/23/26	0/1/1/1
3	NAG	A	2585	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	2586	3	-	0/6/23/26	0/1/1/1
5	NAG	A	2943	1,5	-	0/6/23/26	0/1/1/1
5	NDG	A	2944	5	-	0/6/23/26	0/1/1/1
3	NAG	A	2950	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	2951	3	-	0/6/23/26	0/1/1/1
5	NAG	B	3559	2,5	-	0/6/23/26	0/1/1/1
5	NDG	B	3560	5	-	0/6/23/26	0/1/1/1
5	NAG	B	3654	2,5	-	0/6/23/26	1/1/1/1
5	NDG	B	3655	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2044	NAG	C3-C2-N2	-2.32	108.23	111.76

There are no chirality outliers.

There are no torsion outliers.

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2045	NAG	C1-C2-C3-C4-C5-O5
5	B	3654	NAG	C1-C2-C3-C4-C5-O5

## 5.6 Ligand geometry

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected

value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	NAG	A	2260	1	12,14,15	0.34	0	15,19,21	0.69	0
4	NAG	A	2458	1	12,14,15	0.43	0	15,19,21	0.58	0
4	NAG	B	3320	2	12,14,15	0.35	0	15,19,21	0.66	0
4	NAG	B	3371	2	12,14,15	0.40	0	15,19,21	0.66	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	2260	1	-	0/6/23/26	1/1/1/1
4	NAG	A	2458	1	-	0/6/23/26	0/1/1/1
4	NAG	B	3320	2	-	0/6/23/26	1/1/1/1
4	NAG	B	3371	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2260	NAG	C1-C2-C3-C4-C5-O5
4	B	3320	NAG	C1-C2-C3-C4-C5-O5

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.